```
> O <
Ol IO   Intelligenetics
> O <
```

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-778-187b-1.res made by jdelaval on Fri 17 Jan 103 13:24:27-PST.

Query sequence being compared:us-09-778-187B-1 (1-1598)
Number of sequences searched: 1
Number of scores above cutoff: 1

Results of the initial comparison of US-09-778-187B-1 (1-1598) with:
File : 09-944907.seq

```
100-

 50-
     ·

  0-
     ·
 10-
     ·
  5-
     ·
SCORE    STDEV
```

SCORE	0	149	298	448	597	746	895	1045	1194	1343

STDEV

```
O |-
F |-10-
O |-
R |-
B |-
E |-
M |-50-
U |-
N |-
 |-
 |100-
```

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Scores:

Randomization group
Cutoff score   0
Gap size penalty   0.33
Gap penalty   1.00
Mismatch penalty   1
Similarity matrix   Unitary

PARAMETERS
K-tuple   4
Joining penalty   30
Window size   32.

Times:
              CPU   Total Elapsed
        00:00:00.00   00:00:00.00

Number of residues: 1413
Number of sequences searched: 1
Number of scores above cutoff: 1

SEARCH STATISTICS

Scores:
        Mean   Median   Standard Deviation
        1343   0   0.00

	Mean	Median	Standard Deviation
	1343	0	0.00

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. US-09-778-187B-1 (1-1598)						
US-09-944-907-60	Sequence 60, Application US/09944907	1413	1343	1400	0.00	0

1. US-09-778-187B-1 (1-1598)
   US-09-944-907-60 Sequence 60, Application US/09944907

Sequence 60, Application US/09944907
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kljavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,907
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 60
LENGTH: 1413
TYPE: DNA
ORGANISM: Homo Sapien

Initial Score	= 1343	Optimized Score = 1400	Significance = 0.00
Residue Identity	= 99%	Matches = 1404	Mismatches = 3
Gaps	= 7	Conservative Substitutions	= 0

```
           10        20        30        40        50        60
X     GCG-GCCGCGCCCGACATGGCGAGTGTAGTGCCTGCCGAGCGGGATCCCAGTGTGCGGCGCCGCAGCGGCG
      |||·||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CGGACGGCGTGGGGTGCCCGACAATGGCGAGTGTAGTGCCTGCCGAGCGGGATCCCAGTGTGCGGCGCCGCAGCGGCG
X  10          20          30          40          50          60

           70        80        90       100       110       120       130
GCGGCGGGGGCGGCCTCCCGGGGGCTCCGGCTCCCTCGCTGTTGGCTTCTTCCGGGGCCCGCCGGGGCCCCACA
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GCGGCGGGGGCGGCCTCCCGG-----GGCTCCGGCTCCCTCGCTGTTGGCTTCTTCCGGGGCCCGCCGGGGCCCCACA
     80          90         100         110         120         130

          140       150       160       170       180       190       200
GGTGATGGGCAGAAATCTGTTTACGAAAGACGTGACAGTGATCGAGGGAGAGGTTCGGACCATCAGTTGCCAA
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GGTGATGGGCAGAAATCTGTTTACGAAAGACGTGACAGTGATCGAGGGAGAGGTTCGGACCATCAGTTGCCAA
  140         150         160         170         180         190         200

          210       220       230       240       250       260       270
GTCAATAAGAGTGACGACACTCTGTGATTCAGCTACTGACTGACTCCAACAGGCAGACCATTTATTTCAGGGAC
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GTCAATAAGAGTGACGACACTCTGTGATTCAGCTACTGACTGACTCCAACAGGCAGACCATTTATTTCAGGGACTTC
  210         220         230         240         250         260         270

          280       290       300       310       320       330       340
AGGGCCTTTGAAGGACAGCAGGTTTCAGTTGCTGAATTTTCTAGCAGTGAACTCAAAGTATCATTGACAAAC
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AGGGCCTTTGAAGGACAGCAGGTTTCAGTTGCTGAATTTTCTAGCAGTGAACTCAAAGTATCATTGACAAAC
  280         290         300         310         320         330         340

          350
       350
```

```
360        370        380        390        400        410        420
GTCTCAAATTCTGATGAAGGAAGGAAGATACTTTTTGCCAGCTGCTCTATACCGATCCCCACAGGAGAAAGTTACACCACC
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GTCTCAAATTCTGATGAAGGAAGGAAGATACTTTTTGCCAGCTGCTCTATACCGATCCCCACAGGAGAAAGTTACACCACC
360        370        380        390        400        410        420

430        440        450        460        470        480        490
ATCACAGTTCCTGGTCCCACCACCAACGTAATTCTGATGATCGATATCCAGAAAGACACTGCGCGTGGAAGGTGAGGAG
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATCACAGTTCCTGGTCCCACCACCAACGTAATTCTGATGATCGATATCCAGAAAGACACTGCGCGTGGAAGGTGAGGAG
430        440        450        460        470        480        490

500        510        520        530        540        550        560        570
ATTGAAGTCAACTGCACTGCTATGGCCAGCAAGCCACCAGCACTATCAGGTGGTTCAAAGGGAACACAGAG
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATTGAAGTCAACTGCACTGCTATGGCCAGCAAGCCACCAGCACTATCAGGTGGTTCAAAGGGAACACAGAG
500        510        520        530        540        550        560        570

580        590        600        610        620        630        640
CTAAAAGGCAAAATCGGAGGTGGTCAGAGCATGTACACTGTGACCAGTCACTGACTGAAGGTG
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CTAAAAGGCAAAATCGGAGGTGGTCAGAGCATGTACACTGTGACCAGTCACTGACTGAAGGTG
580        590        600        610        620        630        640

650        660        670        680        690        700        710
CACAAGGAGGAGGACGATGGGGGTTCCCAGTGATCTGCGCAGTGGGACCACCCTGCCGGTCACTGGAAACCTGCAGACC
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CACAAGGAGGAGGACGATGGGGGTTCCCAGTGATCTGCGCAGTGGGACCACCCTGCCGGTCACTGGAAACCTGCAGACC
650        660        670        680        690        700        710

720        730        740        750        760        770        780
CAGCGGTATCTAGAAGTACAGATTATAAGCCTCAAAGTGCACATTCAGATGACTTAATCCTTCTACAAGGCTTAACC
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CAGCGGTATCTAGAAGTACAGATTATAAGCCTCAAAGTGCACATTCAGATGACTTAATCCTTCTACAAGGCTTAACC
720        730        740        750        760        770        780

790        800        810        820        830        840        850
CGGGAAGGGGACGGCGCTTGAGTTAACATGTGAAGCCATCGGGGAAGCCCCAGCCCTGTGATGGTTAACTTGGGTG
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CGGGAAGGGGACGGCGCTTGAGTTAACATGTGAAGCCATCGGGGAAGCCCCAGCCCTGTGATGGTTAACTTGGGTG
790        800        810        820        830        840        850

860        870        880        890        900        910        920        930
AGAGTCGATGATGAAAATGCCTCAACACGCCGTACTGTCTGGGCCCCAACCTGTTCATCAATAACCTAAACAAA
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AGAGTCGATGATGAAAATGCCTCAACACGCCGTACTGTCTGGGCCCCAACCTGTTCATCAATAACCTAAACAAA
860        870        880        890        900        910        920        930

940        950        960        970        980        990        1000
ACAGATAAATGGTACAATACCGCTGTGAAGCTTCAAACATAGTGGGGAAAGCTCACTCGGATTATAATGCTGTAT
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ACAGATAAATGGTACAATACCGCTGTGAAGCTTCAAACATAGTGGGGAAAGCTCACTCGGATTATAATGCTGTAT
940        950        960        970        980        990        1000

1010       1020       1030       1040       1050       1060       1070
GTATACGATCCCCCACAAACTATCCCTCCTCCCACAACACCACCACCACCACCACCACCACCACCACCACCACC
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GTATACGATCCCCCACAAACTATCCCTCCTCCCACAACACCACCACCACCACCACCACCACCACCACCACCACC
1010       1020       1030       1040       1050       1060       1070

1080       1090       1100       1110       1120       1130       1140
ATCCTTACCATCATCACAGATTCCCGAGCAGGTGAAGAGGCTCGATCAGGGACTGGGATCACACCCGTGATC
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATCCTTACCATCATCACAGATTCCCGAGCAGGTGAAGAGGCTCGATCAGGGACTGGGATCACACCCGTGATC
1080       1090       1100       1110       1120       1130       1140

1150       1160       1170       1180       1190       1200       1210
GGTGGCGGTCCGTGGCGGTGGTGGTTCGCCATGCTGTGCTTCATCAATCATTCTGGGGCGGCGCTATTTTGCCAGA
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GGTGGCGGTCCGTGGCGGTGGTGGTTCGCCATGCTGTGCTTCATCAATCATTCTGGGGCGGCGCTATTTTGCCAGA
1150       1160       1170       1180       1190       1200       1210
```

```
1220       1230       1240       1250       1260       1270       1280       1290
CATAAAGGTACATACTTCACTCATGAAGCCAAAGGAGCCGATGACGCAGCAGACACAGCAGCTATAATC
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CATAAAGGTACATACTTCACTCATGAAGCCAAAGGAGCCGATGACGCAGCAGACACAGCAGCTATAATC
1220       1230       1240       1250       1260       1270       1280

1300       1310       1320       1330       1340       1350       1360
AATGCCAGAAGGAGGACAGAACACTCCGAAGAAAAGAAAGAGAGTACTTCATCTGTAGAATCAGCCCTTTTTTGTTTTCA
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AATGCCAGAAGGAGGACAGAACACTCCGAAGAAAAGAAAGAGAGTACTTCATCTGTAGAATCAGCCCTTTTTTGTTTTCA
1300       1310       1320       1330       1340       1350       1360

1370       1380       1390       1400    1410 x    1420       1430
ATGAGGTGTCCAACTGGCCCTATTTTAGATGATGAAAGAGACAGTGATAATTGGGAACTTGCCGAGAAAATTCGTGTG
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATGAGGTGTCCAACTGGCCCTATTTTAGATGATGAAAGAGACAGTGATAATTGGGAACTTGCCGAGAAAATTCGTGTG
1370       1380       1390       1400    1410 x

1440       1450       1460       1470       1480       1490       1500
TTTTTTATGAAATGGGTGGAAAGGTGTGAGACTGGGAGGCTTGGGATTTGCTGTGTAAAAAAAAAAAAA
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TTTTTTATGAAATGGGTGGAAAGGTGTGAGACTGGGAGGCTTGGGATTTGCTGTGTAAAAAAAAAAAAA
1440       1450       1460       1470       1480       1490       1500

1510       1520       1530       1540       1550       1560       1570
ATGTTCTTTGGAAAGAAAAAGCGGGCCGCTTTCTTATTCTATTTCAACATTCAGCTTAAATCATAAATCCTAAA
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATGTTCTTTGGAAAGAAAAAGCGGGCCGCTTTCTTATTCTATTTCAACATTCAGCTTAAATCATAAATCCTAAA
1510       1520       1530       1540       1550       1560       1570

1580
ATCATACATGCTATTTCCAT
1590
```

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-778-187b-2.res made by jdelaval on Fri 17 Jan 103 13:23:42-PST.

Query sequence being compared: US-09-778-187B-2 (1-442)
Number of sequences searched: 1
Number of scores above cutoff: 1

Results of the initial comparison of US-09-778-187B-2 (1-442) with:
File : 09-944907.pep

```
> O <
O| |O  Intelligenetics
> O <

N  100-
U       |
M   50-                                            .
B       |
E       |
R   10-                                   .
    |
O    5-                             .
F       |                    .
S       |       .      .
E    0-|----|----|----|----|----|----|----|----|----|----
Q       0   47   94  141  188  235  282  329  376  423
U                                                    *
E
N     SCORE
C     STDEV
E
S
```

SEARCH STATISTICS

Scores: Mean   Median   Standard Deviation
                   423   0   0.00

Times: CPU   Total Elapsed
               00:00:00.00   00:00:00.00

PARAMETERS

Similarity matrix   Unitary   K-tuple   2
Mismatch penalty   1.00   Joining penalty   20
Gap penalty   0.05   Window size   32
Gap size penalty   0.05
Randomization group   0
Cutoff score   0

Number of residues: 440
Number of sequences searched: 1
Number of scores above cutoff: 1

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. US-09-944-907-61	Sequence 61, Application	440	423	439	0.00	0

1. US-09-778-187b-2 (1-442)
   US-09-944-907-61 Sequence 61, Application US/09944907

GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kljavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,907
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
TYPE: PRT
ORGANISM: Homo Sapien

Initial Score   = 423   Optimized Score = 439   Significance = 0.00
Residue Identity = 99%   Matches = 440   Mismatches = 0
Gaps = 2   Conservative Substitutions = 0

```
X        10        20        30        40        50        60        70
MASVVLPSGSQCAAAAAAAAAPPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDS
|||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
MASVVLPSGSQCAAAAAAAAPPG--LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDS
X        10        20        30

         80        90       100       110       120       130       140
VIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPP
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
VIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPP
         80        90       100       110       120       130       140

        150       160       170       180       190       200       210
RNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGV
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
RNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGV
        150       160       170       180       190       200       210

        220       230       240       250       260       270       280
PVICQVEHPAVTGNLQTQRVLEVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMP
|||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
PVICQVEHPAVTGNLQTQRVLEVQXPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMP
        220       230       240       250       260       270       280

        290       300       310       320       330       340       350
QHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTD
||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
QHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYMLVYVYDPPTIPPPTTTTTTTTTTTTTTTITTTD
        290       300       310       320       330       340       350
```

```
            370        380        390        400        410        420        430
360 SRAGEEGSIRAVDHAVIGGVVAVVFAMLCLLILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQN
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
360 SRAGEEGSIRAVDHAVIGGVVAVVFAMLCLLILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQN
            370        380        390        400        410        420        430

    440 X
NSEEKKEYFI
||||||||||
NSEEKKEYFI
    440
```